



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2016 – 06:47 PM EDT

PDB ID : 5FPV
Title : Crystal structure of human JMJD2A in complex with compound KDOAM20A
Authors : Srikannathasan, V.; Gileadi, C.; von Delft, F.; Arrowsmith, C.H.; Bountra, C.;
Edwards, A.; Oppermann, U.
Deposited on : 2015-12-03
Resolution : 2.44 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027790

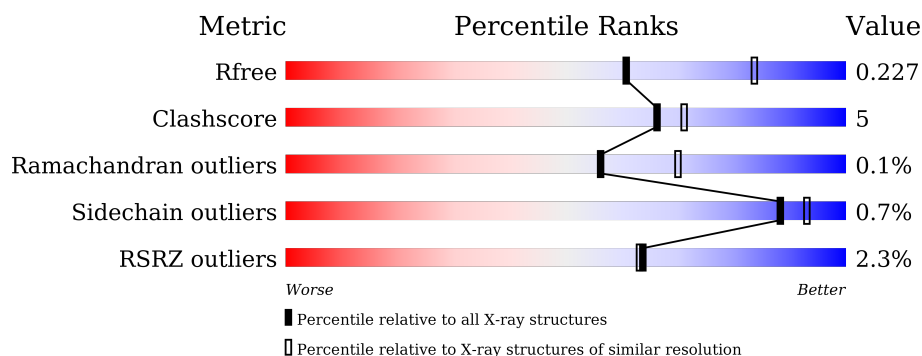
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1003 (2.46-2.42)
Clashscore	102246	1071 (2.46-2.42)
Ramachandran outliers	100387	1065 (2.46-2.42)
Sidechain outliers	100360	1065 (2.46-2.42)
RSRZ outliers	91569	1005 (2.46-2.42)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	360	<div> <div>87%</div> <div>6% • 6%</div> </div>
1	B	360	<div> <div>2%</div> <div>87%</div> <div>8% 5%</div> </div>
1	C	360	<div> <div>2%</div> <div>86%</div> <div>9% 5%</div> </div>
1	D	360	<div> <div>2%</div> <div>89%</div> <div>5% • 5%</div> </div>
1	E	360	<div> <div>3%</div> <div>88%</div> <div>7% 5%</div> </div>
1	F	360	<div> <div>4%</div> <div>83%</div> <div>11% • 5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	360	<div><div><div></div><div></div><div></div></div><div>3%89%6% • 5%</div></div>
1	H	360	<div><div><div></div><div></div><div></div></div><div>%86%7% • 6%</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 23005 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called LYSINE-SPECIFIC DEMETHYLASE 4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	337	Total	C	N	O	S	0	0	0
			2703	1761	445	482	15			
1	B	343	Total	C	N	O	S	0	1	0
			2751	1792	452	493	14			
1	C	342	Total	C	N	O	S	0	0	0
			2739	1782	450	492	15			
1	D	342	Total	C	N	O	S	0	0	0
			2744	1787	452	490	15			
1	E	341	Total	C	N	O	S	0	0	0
			2731	1778	449	489	15			
1	F	342	Total	C	N	O	S	0	0	0
			2747	1788	452	492	15			
1	G	343	Total	C	N	O	S	0	0	0
			2754	1791	455	493	15			
1	H	340	Total	C	N	O	S	0	0	0
			2738	1781	452	490	15			

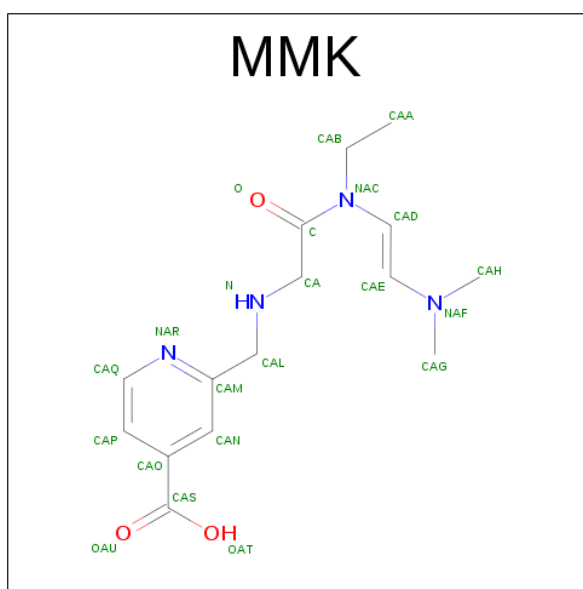
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	EXPRESSION TAG	UNP O75164
B	1	SER	-	EXPRESSION TAG	UNP O75164
C	1	SER	-	EXPRESSION TAG	UNP O75164
D	1	SER	-	EXPRESSION TAG	UNP O75164
E	1	SER	-	EXPRESSION TAG	UNP O75164
F	1	SER	-	EXPRESSION TAG	UNP O75164
G	1	SER	-	EXPRESSION TAG	UNP O75164
H	1	SER	-	EXPRESSION TAG	UNP O75164

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		
2	E	1	Total	Mn	0	0
			1	1		
2	H	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		
2	A	1	Total	Mn	0	0
			1	1		
2	F	1	Total	Mn	0	0
			1	1		

- Molecule 3 is 2-[[[(2-[(E)-2-(DIMETHYLAMINO)ETHENYL](ETHYL)AMINO}-2-OXOETHYL)AMINO]METHYL}PYRIDINE-4-CARBOXYLIC ACID (three-letter code: MMK) (formula: C₁₅H₂₂N₄O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			22	15	4	3		
3	B	1	Total	C	N	O	0	0
			22	15	4	3		
3	C	1	Total	C	N	O	0	0
			22	15	4	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			22	15	4	3		
3	E	1	Total	C	N	O	0	0
			22	15	4	3		
3	F	1	Total	C	N	O	0	0
			22	15	4	3		
3	G	1	Total	C	N	O	0	0
			22	15	4	3		
3	H	1	Total	C	N	O	0	0
			22	15	4	3		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		
4	E	1	Total	Zn	0	0
			1	1		
4	H	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		
4	C	1	Total	Zn	0	0
			1	1		
4	A	1	Total	Zn	0	0
			1	1		
4	F	1	Total	Zn	0	0
			1	1		

- Molecule 5 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	1	Total	Ni	0	0
			1	1		
5	D	3	Total	Ni	0	0
			3	3		
5	H	4	Total	Ni	0	0
			4	4		
5	B	2	Total	Ni	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total 2	Ni 2	0	0
5	A	3	Total 3	Ni 3	0	0


- Molecule 6 is water.

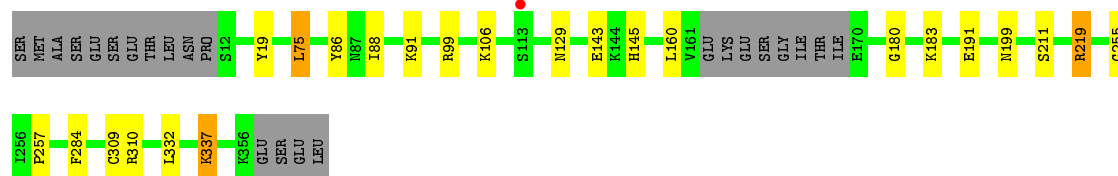
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	135	Total 135	O 135	0	0
6	B	128	Total 128	O 128	0	0
6	C	129	Total 129	O 129	0	0
6	D	121	Total 121	O 121	0	0
6	E	95	Total 95	O 95	0	0
6	F	91	Total 91	O 91	0	0
6	G	72	Total 72	O 72	0	0
6	H	120	Total 120	O 120	0	0

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

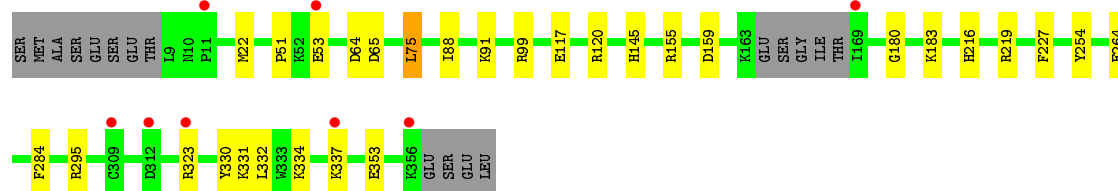
- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

Chain A: 




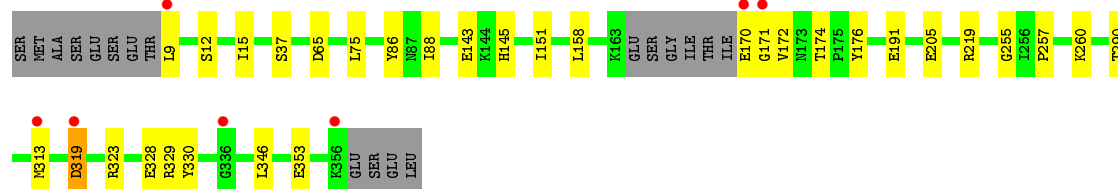
- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

Chain B: 




- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

Chain C: 




- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

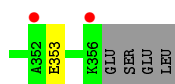
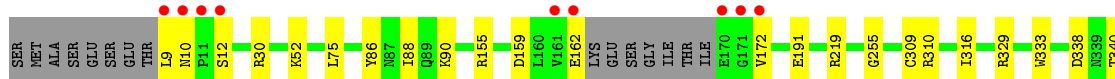
Chain D: 




GLU
LEU

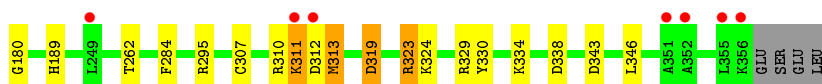
- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

Chain E: 




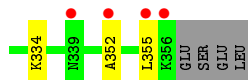
- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

Chain F: 




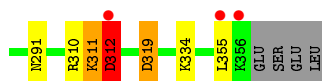
- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

Chain G: 



- Molecule 1: LYSINE-SPECIFIC DEMETHYLASE 4A

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	111.35Å 103.51Å 157.10Å 90.00° 106.37° 90.00°	Depositor
Resolution (Å)	85.33 – 2.44 85.33 – 2.44	Depositor EDS
% Data completeness (in resolution range)	98.5 (85.33-2.44) 91.4 (85.33-2.44)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.45Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.196 , 0.229 0.193 , 0.227	Depositor DCC
R_{free} test set	5764 reflections (4.95%)	DCC
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	23005	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.50 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.4134e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NI, ZN, MN, MMK

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.32	0/2788	0.50	0/3786
1	B	0.36	0/2837	0.55	1/3855 (0.0%)
1	C	0.33	0/2825	0.53	2/3839 (0.1%)
1	D	0.54	5/2830 (0.2%)	0.60	7/3843 (0.2%)
1	E	0.31	0/2817	0.50	0/3828
1	F	0.32	0/2833	0.54	0/3847
1	G	0.30	0/2840	0.51	1/3857 (0.0%)
1	H	0.34	0/2824	0.53	3/3835 (0.1%)
All	All	0.36	5/22594 (0.0%)	0.53	14/30690 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1
1	F	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	334	LYS	CE-NZ	13.32	1.82	1.49
1	D	330	TYR	CE2-CZ	-9.35	1.26	1.38
1	D	331	LYS	CA-CB	9.26	1.74	1.53
1	D	334	LYS	CD-CE	6.17	1.66	1.51
1	D	334	LYS	CB-CG	-5.21	1.38	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	312	ASP	CB-CG-OD1	7.97	125.47	118.30
1	D	334	LYS	CD-CE-NZ	6.65	126.99	111.70
1	C	319	ASP	CB-CG-OD1	-6.40	112.54	118.30
1	B	75	LEU	CA-CB-CG	-6.14	101.17	115.30
1	H	312	ASP	CB-CG-OD2	-5.90	112.99	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	9	LEU	Peptide
1	F	9	LEU	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2703	0	2560	24	0
1	B	2751	0	2602	36	0
1	C	2739	0	2583	28	0
1	D	2744	0	2603	32	0
1	E	2731	0	2579	14	0
1	F	2747	0	2605	35	0
1	G	2754	0	2607	21	0
1	H	2738	0	2599	29	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	22	0	21	1	0
3	B	22	0	21	1	0
3	C	22	0	21	1	0
3	D	22	0	21	1	0
3	E	22	0	21	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	22	0	21	1	0
3	G	22	0	21	0	0
3	H	22	0	21	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	3	0	0	0	0
5	G	1	0	0	0	0
5	H	4	0	0	0	0
6	A	135	0	0	5	0
6	B	128	0	0	14	0
6	C	129	0	0	8	0
6	D	121	0	0	5	1
6	E	95	0	0	1	0
6	F	91	0	0	2	1
6	G	72	0	0	2	0
6	H	120	0	0	4	0
All	All	23005	0	20906	208	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 208 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:334:LYS:CE	1:D:334:LYS:NZ	1.82	1.39
1:D:331:LYS:HA	1:D:334:LYS:HG3	1.37	1.05
1:D:331:LYS:HA	1:D:334:LYS:HE2	1.30	1.05
1:B:330:TYR:O	6:B:2125:HOH:O	1.81	0.98
1:H:311:LYS:O	1:H:312:ASP:HB3	1.61	0.97

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:2102:HOH:O	6:F:2068:HOH:O[2_645]	2.10	0.10

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	333/360 (92%)	328 (98%)	5 (2%)	0	100	100
1	B	340/360 (94%)	332 (98%)	8 (2%)	0	100	100
1	C	338/360 (94%)	332 (98%)	6 (2%)	0	100	100
1	D	338/360 (94%)	330 (98%)	8 (2%)	0	100	100
1	E	337/360 (94%)	331 (98%)	6 (2%)	0	100	100
1	F	338/360 (94%)	328 (97%)	9 (3%)	1 (0%)	46	56
1	G	339/360 (94%)	336 (99%)	3 (1%)	0	100	100
1	H	336/360 (93%)	329 (98%)	6 (2%)	1 (0%)	46	56
All	All	2699/2880 (94%)	2646 (98%)	51 (2%)	2 (0%)	56	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	312	ASP
1	F	311	LYS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	274/316 (87%)	271 (99%)	3 (1%)	80	87
1	B	279/316 (88%)	279 (100%)	0	100	100
1	C	278/316 (88%)	277 (100%)	1 (0%)	93	96
1	D	279/316 (88%)	278 (100%)	1 (0%)	93	96
1	E	277/316 (88%)	277 (100%)	0	100	100
1	F	280/316 (89%)	277 (99%)	3 (1%)	80	87
1	G	280/316 (89%)	277 (99%)	3 (1%)	80	87
1	H	280/316 (89%)	276 (99%)	4 (1%)	74	84
All	All	2227/2528 (88%)	2212 (99%)	15 (1%)	88	93

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	319	ASP
1	F	323	ARG
1	H	173	ASN
1	F	313	MET
1	H	91	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 39 ligands modelled in this entry, 31 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	MMK	A	1358	2	18,22,22	2.75	4 (22%)	17,28,28	3.71	6 (35%)
3	MMK	B	1358	2	18,22,22	2.70	4 (22%)	17,28,28	3.63	9 (52%)
3	MMK	C	1358	2	18,22,22	2.56	4 (22%)	17,28,28	5.68	7 (41%)
3	MMK	D	1358	2	18,22,22	2.72	4 (22%)	17,28,28	4.32	7 (41%)
3	MMK	E	1358	2	18,22,22	2.70	4 (22%)	17,28,28	5.19	7 (41%)
3	MMK	F	1358	2	18,22,22	2.72	4 (22%)	17,28,28	5.74	6 (35%)
3	MMK	G	1358	2	18,22,22	2.64	4 (22%)	17,28,28	3.25	6 (35%)
3	MMK	H	1358	2	18,22,22	2.71	4 (22%)	17,28,28	4.14	6 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MMK	A	1358	2	-	1/17/21/21	0/1/1/1
3	MMK	B	1358	2	-	1/17/21/21	0/1/1/1
3	MMK	C	1358	2	-	1/17/21/21	0/1/1/1
3	MMK	D	1358	2	-	1/17/21/21	0/1/1/1
3	MMK	E	1358	2	-	1/17/21/21	0/1/1/1
3	MMK	F	1358	2	-	2/17/21/21	0/1/1/1
3	MMK	G	1358	2	-	1/17/21/21	0/1/1/1
3	MMK	H	1358	2	-	1/17/21/21	0/1/1/1

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1358	MMK	CAL-CAM	-6.77	1.38	1.51
3	H	1358	MMK	CAL-CAM	-6.48	1.39	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	1358	MMK	CAL-CAM	-6.36	1.39	1.51
3	D	1358	MMK	CAL-CAM	-6.26	1.39	1.51
3	B	1358	MMK	CAL-CAM	-5.88	1.40	1.51

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1358	MMK	CAH-NAF-CAE	-19.76	98.12	121.51
3	C	1358	MMK	CAG-NAF-CAE	-18.89	99.15	121.51
3	E	1358	MMK	CAH-NAF-CAE	-17.69	100.57	121.51
3	D	1358	MMK	CAG-NAF-CAE	-15.16	103.57	121.51
3	H	1358	MMK	CAH-NAF-CAE	-14.63	104.19	121.51

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	1358	MMK	CAD-CAE-NAF-CAH
3	A	1358	MMK	CA-C-NAC-CAB
3	E	1358	MMK	CA-C-NAC-CAB
3	B	1358	MMK	CA-C-NAC-CAB
3	H	1358	MMK	CA-C-NAC-CAB

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1358	MMK	1	0
3	B	1358	MMK	1	0
3	C	1358	MMK	1	0
3	D	1358	MMK	1	0
3	E	1358	MMK	2	0
3	F	1358	MMK	1	0
3	H	1358	MMK	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	337/360 (93%)	-0.01	1 (0%) 94 95	19, 31, 66, 97	0
1	B	343/360 (95%)	0.09	8 (2%) 64 63	19, 31, 69, 123	0
1	C	342/360 (95%)	0.08	7 (2%) 68 68	21, 32, 71, 120	0
1	D	342/360 (95%)	0.01	6 (1%) 71 70	21, 31, 64, 106	0
1	E	341/360 (94%)	0.12	11 (3%) 51 49	25, 39, 66, 125	0
1	F	342/360 (95%)	0.23	15 (4%) 38 37	25, 41, 68, 125	0
1	G	343/360 (95%)	0.22	9 (2%) 59 59	24, 40, 66, 115	0
1	H	340/360 (94%)	0.05	5 (1%) 76 77	19, 31, 54, 116	0
All	All	2730/2880 (94%)	0.10	62 (2%) 64 63	19, 35, 67, 125	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	171	GLY	7.1
1	C	356	LYS	6.9
1	F	171	GLY	6.2
1	D	171	GLY	5.6
1	F	356	LYS	5.4

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	ZN	B	1359	1/1	0.59	0.26	1.66	82,82,82,82	0
3	MMK	H	1358	22/22	0.95	0.21	1.46	21,28,40,45	0
3	MMK	A	1358	22/22	0.96	0.17	1.24	16,21,43,43	0
3	MMK	B	1358	22/22	0.96	0.19	1.14	17,24,38,39	0
3	MMK	E	1358	22/22	0.93	0.22	0.74	36,38,54,57	0
3	MMK	G	1358	22/22	0.96	0.18	0.58	26,34,47,49	0
3	MMK	D	1358	22/22	0.91	0.20	0.36	20,29,47,49	0
3	MMK	F	1358	22/22	0.92	0.21	0.32	36,40,52,53	0
3	MMK	C	1358	22/22	0.94	0.18	0.06	18,33,44,47	0
4	ZN	H	1359	1/1	1.00	0.13	-1.08	35,35,35,35	0
4	ZN	G	1359	1/1	0.99	0.10	-1.28	41,41,41,41	0
4	ZN	A	1359	1/1	0.99	0.11	-1.32	38,38,38,38	0
4	ZN	E	1359	1/1	0.99	0.09	-1.59	38,38,38,38	0
4	ZN	C	1359	1/1	0.99	0.08	-1.89	46,46,46,46	0
4	ZN	D	1359	1/1	0.99	0.10	-1.91	39,39,39,39	0
4	ZN	F	1359	1/1	0.99	0.09	-1.97	38,38,38,38	0
5	NI	D	1362	1/1	0.79	0.10	-2.62	103,103,103,103	0
5	NI	A	1362	1/1	0.90	0.08	-2.77	85,85,85,85	0
5	NI	H	1362	1/1	0.64	0.11	-	103,103,103,103	0
5	NI	H	1361	1/1	0.89	0.14	-	120,120,120,120	0
5	NI	B	1360	1/1	0.94	0.13	-	73,73,73,73	0
5	NI	A	1361	1/1	0.90	0.11	-	87,87,87,87	0
5	NI	C	1361	1/1	0.98	0.12	-	62,62,62,62	0
5	NI	H	1363	1/1	0.38	0.16	-	119,119,119,119	0
2	MN	F	1357	1/1	1.00	0.15	-	27,27,27,27	0
2	MN	G	1357	1/1	0.99	0.12	-	23,23,23,23	0
5	NI	B	1361	1/1	0.98	0.15	-	69,69,69,69	0
5	NI	C	1360	1/1	0.75	0.17	-	90,90,90,90	0
5	NI	G	1360	1/1	0.95	0.17	-	65,65,65,65	0
5	NI	D	1360	1/1	0.97	0.13	-	64,64,64,64	0
2	MN	D	1357	1/1	0.99	0.13	-	18,18,18,18	0
2	MN	A	1357	1/1	1.00	0.15	-	20,20,20,20	0
2	MN	E	1357	1/1	1.00	0.15	-	26,26,26,26	0
2	MN	B	1357	1/1	1.00	0.13	-	17,17,17,17	0
5	NI	H	1360	1/1	0.98	0.20	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	MN	H	1357	1/1	0.99	0.12	-	17,17,17,17	0
5	NI	A	1360	1/1	0.93	0.17	-	65,65,65,65	0
2	MN	C	1357	1/1	1.00	0.11	-	23,23,23,23	0
5	NI	D	1361	1/1	0.86	0.10	-	80,80,80,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.